

FIG. 1A

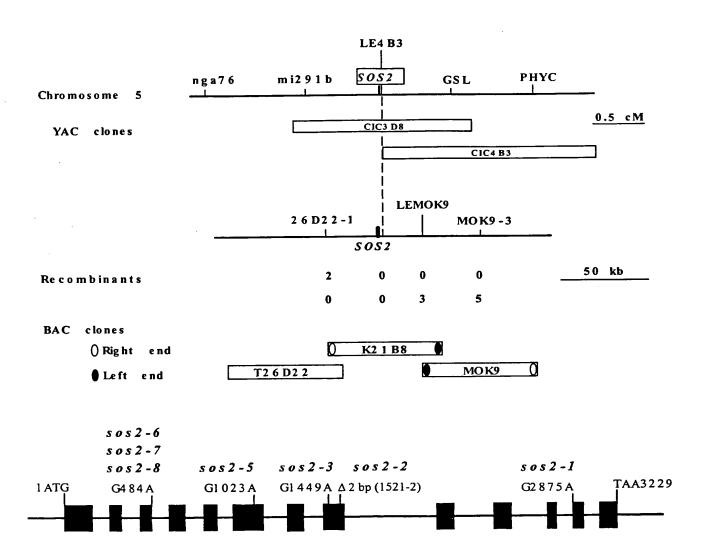


FIG. 1B



FIG. 2A

Kinase Regulatory Domain

FIG. 2B

TOGATCAGATAAAAGTTTGTAAAGA ATCHCAAAGAAAATGAGAAGAGTCOCCAAGTACGAGGTTCGTCCCCACAATACGTGAAGGAACCTTTCCTAACGTTAAGM T K K M R R V G K Y E V G R T 1 % \blacksquare E \blacksquare T F A K \blacksquare K -- I --TTTCCCCACACACACACACTCCTGATAATGTACCCATCAAAATTATCCCTAAGAGTACAATACTTAAGAACAGAATGF A R N T D T G D N V II II II M A K S T I L K N R M -- II --GITGATCAGATAAAAAGAGAGATATCTATAATGAAGATTGTTCGTCACCCGAACATAGTGAGGTTGTATGAGGTGTTG V D Q I K R **II** I S I M K I V R H P N II V R L Y E V L -- III ---- IV--COCGACTICCTTCGAAAATATATATATATTCGAGTTTGTGACAOGACGAGCCTCTTTGATAGAATTGTTCATAAACCG 79 A S P S K I Y I V L E F V T G G E L F D R I V H K G -- V--ACCETTGAAGAAACIICACTICCCGAAATACTITTCAACACCTTGTAGATCCTGTTCCTCATTGTCACTCCAACGGTGTT R L E E S E S R K Y F Q Q L V D $\stackrel{?}{A}$ V A $\stackrel{?}{B}$ $\stackrel{?}{C}$ H C K G V TACCACCHIGACTAAACCCAGAAAATCTTTTACTCGATACAAATCGAAATCTGAAACCTTTCCGATTTCCGACTCAGT
Y R E K P E E L L D T N G N L K V S L S -- VII ---- VIII --CKNACGETT ACCATCGTTCACCACCTGATATTTCGTCTTCCCCGGTTATTCTTTTCGTTATATTCCCTCGATATTTAGC Q G Y D G S A A B I W S C B X 1 L F V I L A G Y L -- IX --CUTTITICOGAGACIGATICTICCACCGITTGTACAGAAAATAAATICAACCAGAGITTTCTTGTCCACCGITGGTTTTCC P F S E T D L P G L Y R K I N A A E F S C P P W F S 209 -- X --CCANACITYTTAATACATACGATACTTGACCCCAATCCCCAAACACGCTATTCAAATTCAAGGAATCAAGAAA A E V K F L I H R $rac{1}{2}$ L D P N P K T R I Q $rac{1}{2}$ Q G I K K -- XI --CATULTITICGTTUACATTAAATTATCTTCCCTATACGACCAACCAACCAACAACAACGAACTTGAATTTCCCATGATATTCCTCCA D P W F R L N Y V P I R A R E E E E V N L D D I R A CITTTTGATGGAATTGACQQCCAGTTATGI ACCCGGAGAATGTAGAGAGAAATGATGAACCCCCCCTGATGATGAATCCC V F D G I E G S Y V A E N V E R N D E G P L M M N A TITGYCATGACTACCCTTAACACCCTTAACATTTATCTCCACTATTTCGACCTCCACCACGATTTTCTTAAACCCCAA F E M I T L S Q G L N L S A L F D R R Q D F V K R Q ACCCGTTTTGFTTCTCCGAAGCGAACCTAGTGAGATAATTCCTAACATTGACCCTGTACCGAACTCAATCCGTTTTAAG TRFVSRREPSEII ANI EAVANS MGFK TCTCATACACCAAACTTCAAGACAACCCTCCACCGATTATCTTCCVTCAACCCCCGACAGITACCTGTTGTGATAGAG S H T R N F K T R L E G L S S I K A G Q L A V V I E 365 ATTT ACCIACOTROCCACCATCCCTTTTCATCGRAGACGTAAGAAACCCTCCTCGGGAAACTCTTGAATATCACAAGGTC Y E V A P S L F M V D V R K A A G E T L E Y H K F TACAAGAACCTATGTTCGAAACTQGAAAACATAATATQGACCCCAACAGAACGAATACCAAAGTCAGAGATTCTCAGA Y K K L C S K L E N I I W R A T E G I P K S E I L R

ACAATCACGITTTTGATCCCAACTTAA







FIG. 3B

SOS2	332 ODFVKROTREVSRR PSELLAN EAVANS EKS TRIFKTRLEGESSIKAGO AV
yCHK1	389 ICPPER TREKSRASRETLIDH YESLRLESISVTMKYVRIQTILYENLH FRKCLIOG
hCHK1	371 RLVKRSTRF BIKLEA KSYQCLKRICEK GOW KSCMNOSTESTER NNKLIFF
SOS2	889 IDEYD ZOPSIF VEVRKAASET DE KEKKI CSKIEN II WRATEGII
yCHK1	149 IDITNI CHNIEI II SIKNSPIE KEKNIVSSIGKPIVLTD SON
hCHK1	28 WALLE D-DKILVOPPISKOG BETWEN IN WSSOK WATE



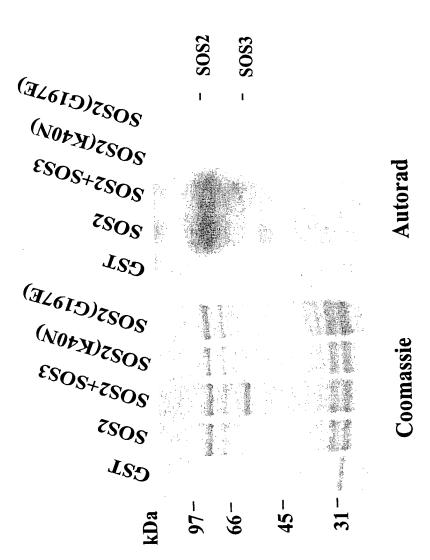


FIG. 4

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